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GenCore version 5.1.3
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February 23, 2003, 21:05:35 ; Search time 3922 Seconds
(without alignments)
10907.987 Million cell updates/sec 1 ggatetttettttteattte......ettttagtttegteaatatg 1470 4109280 Total number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 em\_htg\_inv:\* em\_htg\_other:\* em\_htg\_mus:\*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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PAT 22-JUN-2001 Candida albicans.
Candida albicans
Eukaryota; Fungi, Ascomycota; Saccharomycetina; Saccharomyceteles;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

1 (bases 1 to 1470)
Sandstrom, P.
Methods for altering the expression of hyphal-specific genes Patent: WO 0138550-A 1 31-MAY-2001; linear DNA Sequence 1 from Patent W00138550. AX154641 AX154641.1 GI:14536200 LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS TITLE JOURNAL RESULT 1 AX154641

TURES SOUR	Sundstrom, Paula (US)  Location/Qualifiers  1 1470  /organism="Candida albicans"  /db_xref="taxon:5476"  7509 a 260 c	
GIN	tch 100.0%; Score 1470; DB	
Best Loc Matches	dels	
Oy 1 Db 1	GGATCTTTCTTTTCATTTCCCTTAAAACCGATCAAGAAAGA	
Qy 61 Db 61	GATAAATGTTGATTTTGTGTAATTCAATCAACTAAGCACGTTTGACAGTTAAAAAGTACG 120 	
Qy 121 Db 121	TTGTTGTTGTCCTCGTCTCGTCTAATTTCTGTTGACGAGGATTAATAACAAGAAATACAG 180 	
Qy 181 Db 181	GAAACCTCCAAAAAAAAATTTTGGACCTTACACGCACATAAATTGCGGATAAACTTGC 240 	
Oy 241 Db 241	CATAATAAAAACTCTTTGAAACATACGATATGTTATTCTTTTGATAACTGGAATATTTTT 300	
Qy 301 Db 301	GCTTTTTTTTAACATTATGAACAATTGAAAAAAAAGGAAATGAAAAGGTAAGGTTGCC 360 	
Oy 361 Db 361	TAACCATTGAAATAATAGCTAAGGTTTTCCTGATGCGTTTAACTAAAAAGGAAATAA 420 	
Oy 421 Db 421	CAAAAGTTATTAGCGATAACCTGCGTAAGGTGTCAACAAATATATTTTGCACGTTAGCT 480 	
Qy 481 Db 481	CTATAGAAAATATACAAACTAAATCCTTAAGGAATTTCCTCTATATATA	
Qy 541 Db 541	CTCTCACAGTGAACTGAATTATCCATCTGAATTATCAGTCCACTAATTCCATCAATAAAA 600 	
Qy 601 Db 601	TAGATTAGTGTATTGTTCTCTTCAGTACAATTACTACCATTATGCAATGCTAGCTTATTG 660	
Oy 661 Db 661	TICATAATTAGCCATGTIGCACACCCTAATICGAACATTAACTGTAICCATATTITGTI 720 	
Oy 721 Db 721	GTCCTTCTTTGTTTTTTTCTAACAAAATGTTCCAGAATTTTTTAAAAAATATTTGAAAA 780 	
Qy 781 Db 781	AACACATAACACTTTGAGTAIGATAATATCAACTATTGACTTGTTTTGAAAGTAAAGAT 840 	
Qy 841 Db 841	CAAATTTTTTTTTAGTGGACTAATGCACTTTACATCAACTGGATGTTATTGGATGTAC 900 	
0у 901	tactataaggctcaaacaaattatctttcaaaaatgttataacttaaggtcatctataat 960	

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CAU64206 2682 bp DNA linear PLN 17-DEC-1998 Candida albicans hyphal wall protein 1 (HWP1) gene, complete cds.
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Staab,J.F. and Sundstrom,P.
Genetic organization and sequence analysis of the hypha-specific cell wall protein gene HWPl of Candida albicans
Yeast 14 (7), 681-686 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
1 (bases 1 to 2682)
                                                                  1021 ATTGTAAAAAGGGAAGGTTTTGGTAGGCTCATAATCGTTATAATGTACCTCTAAAGTAA 1080
                                                                                                                                                                                 1141 GATAAGTTAGTTAGCCCAGCTGTTTTTTTTTTCCTTATTTTTTAGACTACATTTGTTT 1200
                                                                                                                                                                                                                                                                                                                                 1201 CACTITITGITGCGACTITAATACCGTITITGCAACTICTCTITGTATCACCTGTATCCG 1260
                                                                                                                                                                                                                                                                                                                                                                                                   1381 ATTTCAATTTCCATTCAACTTGTTTTCTCAACAATATCAAACAACAACAACAACAAGAATCTCCTA 1440
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                                                TCTTTGGATCCAAAAACAAGGAATTCGGAAATTCTGACGATAAATGTCGACTCACAATTC 1020
                                                                                                                 1021 ATTGTAAAAAGGGAGAGTTTTGGTAGGCTCATAATCGCTTATAATGTACCTCTAAAGTAA 1080
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                                                                                                                                                                                                                                                                                                                                                                                  1381 ATTITCAATTICCATTCAACTIGTTTTCTCAACAATATCAAACACAACAGGAATCTCCTA 1440
Stabb.J.F., Ferrer.C.A. and Sundstrom, P.
Developmental expression of a tandemly repeated, proline-and glutamine-rich amino acid motif on hyphal surfaces on Candida
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Staab,J.F. and Sundstrom,P.
Direct Submission
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AUTHORS

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Direct Submission Submitted (17-DEC-1998) Medical Microbiology & Immunology, Ohio State University, 333 West 10th Avenue, Columbus, OH 43210, USA Sequence update by submitter On Dec 17, 1998 this sequence version replaced gi:1915978.
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                                                                                                                      PLN 24-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-MAY-1997) Microbiology and Immunology, Georgetown University, 3900 Reservoir Road NW, Washington, DC 20007-2197, USA On Jul 24, 1997 this sequence version replaced gi:2209195.
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                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
1 (bases 1 to 2188)
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                                                                                                                                    Candida albicans ECE2 gene, complete cds.
                                                                                                                      DNA
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/db_xref="taxon:5476"
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1446 ACTCGCTTTTAGTTTCGTCAATATG 1470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (05-NOV-1998) on behalf of the pilot sequencing project on the Candida albicans strain 1161 genome. Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail:

Barrell@sanger.ac.uk Cosmids supplied by Prof. Duncan Shaw, [3]
Department of Molecular and Cell Biology, The Institute of Medical Science, University of Aberdeen, Foresterhill, Aberdeen, AB25 2ZD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMAPNVVTLLGLFFIIGNLMTVFYYDPYLNETQPTWCYFFYAFGLFMYQTFDGCDGCH
ARRTGQSGPLGELFDHSIDAINTTLGTFVFASVLKMGYGGLLLLSQFASVCNFYTSTW
EEYHTHTLFLSKFSGPVEGILMICIVYIITGIFGPDIWTIDLFELNLTSLGYGYYKVD
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complement(1. .785)
/gene="ca35A5.01c"
/gene="ca35A5.01c"
/note="ca35A5.01c"
/note="ca35A5.01c, partial orf, len: > 261 aa, most
similar to EPTI_YEAST ethanolaminephosphotransferase (EC 2.7.8.1) (391 aa), fasta scores opt: 984, E(): 0, (56.3% identity in 263 aa overlap), contains PS00379 CDP-alcoholphosphatidyltransferases signature"
                                                                                                                                                                     ARS; Canik1; CDP-alcohol phosphatidyltransferase; chitin synthase;
                                                                                                                                                                                             chs1; cytcchrome P450; DNA polymerase delta; histidine kinase; isocitrate dehydrogenase pseudogene; LTR; pol3; Rcc1; regulator of chromosome condensation; rehydrin; RPS1-like region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Funding: sequencing funded by Beowulf Genomics Ltd. CDS are numbered using the following system eg CAC20C1.01c. CA (C. albicans), 20C1 (cosmid name),

10 (first CDS), c (complementary strand).

The more significant matches with motifs in the PROSITE/PFAM database are also included but some of these may be fortuitous. IMPORTANT: This sequence MAX NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid Ca35A5 is likely to map to region R, chromosome 7.
                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
1 (bases 1 to 42565)
Tait, E., Simon,M.C., Kinq,S., Brown. אוני מאש אול פראיי חיד
                                                                                                                                                                                                                                                                                                                                                                                                                              Tait, E., Simon,M.C., King,S., Brown,A.J., Gow,N.A. and Shaw,D.J.
A Candida albicans genome project: cosmid contigs, physical
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/product="putative alcohol phosphatidyl transferase"
/protein_id="CAA21944.1"
                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fungal Genet. Biol. 21 (3), 308-314 (1997)
                                                           DNA
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/strain="1161"
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Barrell, B.G. and Rajandream, M.A.
Direct Submission
                                                           42565 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mapping, and gene isolation
                                                                                  C.albicans cosmid Ca35A5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Article No. FG970983
2 (bases 1 to 42565)
Oliver, K. and Harris, D.
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                                                                                                                                           AL033396.1 GI:3850143
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/translation="MSEVPNQESPSSILKQSNASSSTKVHGAPSSSQIANVDFNTLR
KLNSNTSFSSNLTNSTTNTSNALSRLFTRNKSLSNISVHPSSSDDDSSPKTLRESTSP
SESSKSVSGNRLRIAKKLKFSKNQSSRKPDLFLDTSSTISEDSSSFRKVIIGNSLNEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKPRKSSMSSPMSTTFHSLEHRSHHNGSNLQRDTNOVATGTTPLSGKFDDFSKASKTT
CLGSSNSSNSTISNPELAGYTWTTPNTSIEDRFANLDHTNSSFLDIHKKMLVPADSF
IQNKLNKYRQTGVGLGIYESELDHDNDKIYSNLYHYLKPLFTPSFGISDSQGKSKMR
PILSASVEEIANFVKESFCLHQPNHERSFRSKTRSSVSSLGRDKVEDFDYLQLSNLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CaA21946.1"
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MVEIERLKKANSFYBOSIDKIKEILIVNDQKIDSQNBAFSSLAKKSALKQVDKNYQLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLMSLLSHNLQTTEPSEVSLQALILNAWKYYNAYVRFYLLSIFQPLQIYLNELFTRSH
NGSKIIRIDDLLLVSFRKVFITEQGIGSGERETSQFLGNAESEDLTGNGLLTSTLAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Ca35A5.03, unknown, questionable orf, len: 141 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20359. .20769
//note="BLASTN match (score: 1704 strand: (+1), range: 49-459) to CAARREEE X65035 C.albicans DNA of an autonomously replicating sequence (ARS)"
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/note="BLASTN match (score: 669, strand:(+1), range: 8-175) to AF069450 C. albicans retrotransposon long terminal repeat zeta"
19204. .1927
/note="BLASTN hit (score: 325, strand: (+1), range:
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                                                                                       /note="PS00379 CDP-alcohol phosphatidyltransferases
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405-687) to CAAURESE X65035 C.albicans DNA of an
autonomously replicating sequence (ARS)"
20808. .23888
                                                                                                                                                                                                                                                                                                                                                                                                               /note="Ca35A5.02, unknown, len: 512 aa, possible
TSIIYTIIGLTSLYFNIASAMFNVSKHYKKSSTNNSSSGDKDGS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein"
/protein_id="CAA21945.1"
/db_xref="GI:3850145"
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                                                                                                                  signature"
4307. .11124
/note="RPS1-like region"
complement(7606. .8085)
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                           complement(423. .491)
/gene="Ca35A5.01c"
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/gene="Ca35A5.03"
                                                                                                                                                                                                                                                                                                                                                     13175. .14713
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/transl_table=12
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/transl_table=12
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20808. .23888
/gene="Chs1"
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APVQVLFCLKESNQKKINSHRWLFNAFCPVLDPNVIVLLDVGTKPDNHAIYNLWKAFD
RDSNVAGAAGEIKAMKGKGWINLTNPLVASQNFEYKLSNILDKPLESLFGYISVLPGA
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/gene="Ca35A5.05"
/note="PS00626 Regulator of chromosome condensation (RCC1)
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                                                                                                                                             GKAGNLVLENPVPTELRKVLTRTESPFGEFTNMTYTACTSQPDTFSAEGFTLRAAKYG
RETEIVICITMYNEDEVAFARTMHGVMKNIAHLCSRHKSKIWGKDSWKKVQVIIVADG
                                                                                                                                                                                                                                                                                                  LSAYRYIALKNHDDGTGPLASYFKGEDLLCSHDKDKENTKANFFEANMYLAEDRILCW
                                                                                                                                                                                                                                                                                                                                                                                                                      FGTGGTSTYVLVSIVVSLLSTYGLYTLMSILYLDPWHMLTCSVQYFLMIPSYTCTLQI
FREVNHUPSWGTKGDNNPKEDLSNQY IENNASGEPERAVLYDTNIDEDYLETLYNIR
SKRENKVALGHSEKTPLDGDDSYARDYTRYVLFWMIANLYFIMTWQYYEPGDTGRN
IYLAFILWAVAVLALVRAIGSLGYLIQTYARFVYESKSKWMKROYTAPSHNPLN"
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TRAVENLENEELEVQLAATDNLSAALSNGDYVAWGCRCNGTLGFTKDEIKLOKTP
IKRIKELKNIVQLAAGKDHLLALDSKGIVSWGNGOQOQUGRRILERHRYRSLEPQOFG
LYNIKXIASGDFHCFAIDHSDNVYAWGLNQYGQCALFGDNGELEDGSVLMKPTLIPEL
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TATKNEDIILLIGAGGGFSVSGGVKIEDEEKAEVRLDKYEDLE"
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/gene="Ca35A5.05"
/note="PS00625 Regulator of chromosome condensation (RCC1)
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                                                                                                                    HSEGTAYSGSSYLSDDASPETTDYFGASIDGNIMHNINNGYVPNREKTITKRKVRLVG
                                                                                                                                                                                                                                                                                                                                 ELVSKRNDNWVLKFVKSATGETDVPETIAEFLSQRRRWINGAFFAALYSLYHFRKIWT
                                                                                                                                                                                                                                                                                                                                                              TDHSYARKFWLHVEFIYQLVSLLFSFFSLSNFYLTFYFLTGSLVSYKSLGKKGGFWIF
TLFNYLCIGVLTSLFIVSIGNRPHASKNIFKTLIILLTICALYALVVGFVFVINTIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MVALKREAEPRENGKSKKAKTSLATSSFVLHSYSKLPNINEYAK
AKSTPLDVFVWGTGSMCELGLGPSAKNKEVKRPRLNPYLTEEKLGGTKIVDFAVGGHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHKGIKEIAAGEHHTLALTEDGQVYAWGRYDMKEIGIPKDKLPKSTFKDQHGNPRSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Ca35A5.05" RCC1-11ke gene, len: 492 aa, highly /note="Ca35A5.05, RCC1-11ke gene, len: 492 aa, highly similar to RCC_ANAL RCC1 (464 aa), fasta scores, opt: 2782. E():0, (91.9% identity in 469 aa overlap), contains PS00625 Regulator of chromosome condensation (RCC1) signature, 2 x PS00626 Regulator of chromosome condensation (RCC1) signature 2, contains Pfam match to entry RCC1 PF00415, Regulator of chromosome condensation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35150 TATAGAAAATATATACAATTTAATTTGTGGGAATCTACCCTTTATATAGAAAAAAA 35091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35090 ITCTCTCACAGTGGACTGAATTATCCATGTGAATTATCAGTCCACTTATTCCATCGTCAA 35031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAAAATAGATTAGTGTATTGTTCTCTTCAGTACAATTACTACCATTATGCAATGCTAGCT 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480 TCTATAGAAAATATACAAACTAAATCCTTAAGGA-ATTTCCTCTATATATAATAGGAAAT 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Pfam match to entry RCC1 PF00415, Regulator chromosome condensation (RCC1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=12
/product="regulator of chromosome condensation"
/protein_id="CAA21948.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8; Length 42565;
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75.5%; Pred. No. 6.6e-13;
tive 0; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GI:3850148"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Ca35A5.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Rcc1-like"
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/gene="Ca35A5.05"
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Matches 209;
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join(322. .603,826. .1023,1197. .1301,1458. .2942)
/gene="PFC0575w, MAL3P5.1"
/gene="PFC0575w, MAL3P5.1"
/gene="PFC0575w (MAL3P5.1"
/note="PFC0575w (MAL3P5.1"), Hypothetical protein, len: 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSPQ1YRKRFKRSR1KNVSFKKQKKPLFLFENLKKGFSFLGFWRNQYDQKYIDDVIS
NINNLTRIKQVTHKKKSNEFTKENIKQ1LLHCVFSKIDFKIINNLSYIIKHFQMSNIT
VHSILNQISEKVKEKKDAENYLALHLFLLKDENITLFSMMHIMDFFKSKQKVIECIRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MYLKNVYIYISSCFILFDLCFSFHLLKMKYKNHMNNMKSVTFFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T., Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T., Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S., Hornsby, T., Horrocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J., Moule, S., Mungall, K., Murphy, L., Oliver, K., Quall, M. A., Rutlers, S., Skelton, J., Squares, R., Squares, S., Sulston, J. E., Whitehead, S., Woodward, J.R., Newbold, C. and
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/product="Hypothetical protein, PFC0575w"
/protein_id="CAB38969.2"
/db_xref="G1711065"
/db_xref="SPTREMBL:097258"
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Direct Submission
Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
                                     On or before May 14, 2001 this sequence version replaced gi:2982535, gi:2982556, gi:2984556, gi:2982554, gi:2982552, gi:2982572, gi:2982574, gi:4493931.

For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
1. 86827
                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum MAL3P5, complete sequence.
AL034556 AL008971 AL008972 AL008978 AL010141 AL010153 AL010162
AL010206 AL010210 AL139179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The complete nucleotide sequence of chromosome 3 of Plasmodium
656 TATTGTTCATAATTAGCCATGTTGCACCCCTAA-TTCGAACATTAACTGTATCCATATT 714
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    (bases 1 to 86827)

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                                                                                                                                                                   34910 TGTCGTGTAGTGGTTATCTTTTAAATACGCTGT 34874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; centromere; CTRP protein; initia
Serine/threonine protein phosphatase.
                                                                                                                              715 TTTCTTGTCCTTCTTTGTTTTTTCTAACAAAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum 3D7
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7790. .7799
/gene="PFC0581w"
/note="potential splice acceptor sequence for exon 2 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="potential splice acceptor sequence for exon 4 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon 7 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
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                                                                                                                                                                        /note="potential splice donor sequence for exon 2 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="potential splice donor sequence for exon 7
                                                                                                                                                                                                                                                                                                                                                                              'note="potential splice donor sequence for exon 3
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ONFLKEEKNNSDKLQDDIDEDEEKYFDEEILREAKKKSEEYDKDDEEL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="potential splice donor sequence for exon
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Pred. No. 8.5e-06;
0; Mismatches 813; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="potential splice donor sequence
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/gene="PFC0581w"
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Best Local Similarity 42.0°
Matches 592; Conservative
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9361. .93
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8302. .9368,8568. .8641,8713. .8812,8924. .9006,9122. .9258,
9369. .9505,9613. .9838)
/gene="PFCO581w"
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3302. .886,8568. .8641,8713. .8812,8924. .9006,9122. .9258,
9369. .9555,9613. .9838)
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YPDHINSSRANGSFKALKOOTDDNITKHIIMOGERYPNMKSBOBHEKKNNNTGONINEK
DQKDOILKKIYFKGARKLDDIQILNELYNYTWRLLFBCSLKLISTRKNHHLDEKKWB
PDKDNKIIYLNSADYMNNLRRNILKRFSKNEERENINSFASFPFLLSKNIHLLEKKWB
FDKDNKIIYLNSADYMNNLRRNILKRFSKNEERENINSFASFPFLLSKNIHLGEN
NNNTGSRDYNIYMYDKETWRTYTRNNNNDNDNICSNNDHIGSNNDHIGSN
NNNNTGSNNNNNTGSNNNNNTGSNNNNNTGSNNNNNTGSNNDHIGSN
NNNNTGSNNNNNTGSNNNNNTGSNNNNNTGSNRNNNTGSNRDHIGSN
YELAKIYTNNIFDYLKGKKEKHQNEDNTINLYYIKKFPWIFYLKNIIKNKDISFIEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLYYYNKLDNKHNLINEKKLKYFKQINNEHTQQAPTNHTHHNNNNNKKPLDINIHSC
KNTNISSYSTYNNMEKENINIYDKYNIHNFYTEKSISYKDENCQHITLNMIYLLNQTY
DNICRICLNTNTNIYINFYMINIKYICYKNMEIILLNYNHIEDMKKKINQKNNTNTS
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QKIFHIYFANEQIASSFFESHKNYRVTKEDIIDGIEKCWFNITDYLISESIKQDNDFS
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LKVKDEEIVSKKNNFSFSALSNDSNSVTKKYIVDLTLLDNIIESETKYNFASVGKVVV
TLKKEKKKIWNRLLLSKEKYPNMQVWWDMKEKRIHIITFVTINLFFLLSLSHRYHDSV
                                                                                                                           NVNLDQHGRVKSNDENTKSTEHIKNKNTINKCYDTELIQNQMENNFIKKNIDNNISND
ISNNEINIIKLKKLNQSDEDINLTSDLIYERLRTKVLMYIQKIEYLKFKYQYDIINEQ
YPIIKNEKTVLDLLNYGYKIVMSPDVDNSLFEKTKIDSIPNEKDKNNQMENQKNSKNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="MLGLKRKNVFYLLVSVPSLFAYFLKRHKDNENNYETLINNNDIE
KIKRIRIHNKCSYIPLLFLNIYDSYIYKNKILRMLYFKFRKRRKDKEEYYITINMVRK
KRREAIKYNFISDEQNLFNKFYIYEIVLEYSLKYGILSPHLSLYILKNISEHCVNIYP
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IDIVKFKDLYYCMINNINNIFSYIHKVDHNECVYRIFKAYNKILLYEYNYLNEKENIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNNIVNGDIKNNNIIFKKKYNLFESSIISYFYIKDIYEYNYKLRLYYIYDNLIKKFCR
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                                                                               DDENLKELKDTYEQFQLFNDNIIKYIEEDQPLYNINDNSNINDNNNNINTMKNKHKIK
                                                                                                      DIYNDDDDYDYEKEEDLVIQKNIDDYIYKNTIGMNKSLEEFKNQFIEQADIEFQNFLS
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     IKSKKKRKKNLSIYINLFICTLIYFTYCMCLLIKYISHLCIFFFFFFFFLCYNILER
                                                    FTMKLNIERNNKNIIRSNYDNINNDISIDKDMYMNNPIDVNINNISLDEKIKEQFENP
                             IYEECVGDLIRKKIERYNLYCEKKKIKFHMKDAIKKMEINMKDDDLYFNYHYDELLRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3354. 6644)
/gene="PFC0580c, MAL3P5.2"
/note="PFC0580c (MAL3P5.2), Hypothetical protein, len:
1097 aa, possible signal sequence, predicted using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="PFC0581w, hypothetical protein, len: 324 aa, revised: new gene prediction, splicing prediction very
                                                                                                                                                                                                                                  604. .609
/gene="pFC0575w, MAL3P5.1"
/note="pFc0575w, revised)"
                                                                                                                                                                                                                                                                                                                                                                                      /note="predicted splice acceptor sequence for exon 2 (revised of PFC0575*)"
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/gene="PFC0575w, MAL3P5.1"
/note="predicted splice donor sequence for exon 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="Hypothetical protein, PFC0580c"
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/db_xref="GI:4493932"
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/protein_id="CAB90285.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFC0575w (revised)"
complement(3354. .6644)
/gene="PFC0580c, MAL3P5.2"
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40185 ATTTAATTTAATATTGTATTCAATAATTAAAAAAATATAAATATGTTTCATAAAATA 40126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               960 TICTIIGGAICCAAAAACAAGGAAITCGGAAAITCIGACGAIAAAIGICGACICACAAII 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1080 ATCTAAAACAAACATCTTTCTAAAACCTATAATAATAACCTAAATGGCTCACAACCG 1139
                                                                                                         123 GTTGTTGTCCTCGTCTCGTCTAATTTCTGTTGACGAGGATTAATAACAAGAAATACAGGA 182
                                                                                                                                                                                                                                              243 TAATAAAAACTCTTTGAAACATACGATATGTTATTCTTTTCATAACTGGAATATTTTGC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            663 CATAATTAGCCATGTTGCACACCCTAATTCGAACATTAACTGTATCCATATTTTTTTGT 722
                                                                                                                                                                                                 40665 ААТАТТАТАТАТАТАТАТТАААТТТААТТТТАТТТААТТААТТАААТТАААТТАААТ
                                                                                                                                                                                                                                                                  303 TTTTTTTTAACATTATGAACAATTGAAAAAAAAAGGAAATGAAAAGGTAAGAGTTGCCTA
                                                                                                                                                                                                                                                                                                                                                                                    363 ACCATIGAAAATAATAGGCTAAGGTTTTTCCTGATGCGTTTAACTAAAAAGGAAATAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           423 AAAGTTATTAGCGATAACCTGCGTAAGGTGTCAACAAAATATATTTTGCACGTTAGCTCT
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                                  63 TAAATGTTGATTTTGTGTAATTCAATCAACTAAGCACGTTTGACAGTTAAAAAGTACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              543 CTCACAGTGAACTGAATTATCCATCTGAATTATCAGTCCACTAATTCCATCAATAAAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     780 AAACACATAACACTTTGAGTATGATAATATCAACTATTGACTTGTTTTGAAAGTAAAGAA
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                                                                                                                                                                           183 AACCCTCCAAAAAAAAATTTTGGACCTTACACGCACATAAATTGCGGATAAACTTGCCA
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104992 bp DNA linear HTG 01-APR-1999 Plasmodium falciparum chromosome 12, *** SEQUENCING IN PROGRESS AC005504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 104992) Hyman, Y. Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B., Conway, A.B. and Davis, R.W. Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                               1140 GGATAAGTTAGTTAGCCCAGCTGTTTTTTTTTGCCTTATTTTTATGACTACATTTTGTT 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1200 TCACTITITGITGCGACTTTAATACCGTTTTTGCAACTTCTCTTTGTATCACCTGTATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Apr 2, 1999 this sequence version replaced gi:4337172.
* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 104992)
Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
Direct Submission
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104992: contig of 13781 bp in length.
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/db_xref="taxon:5833"
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73357 AATAAATAAATAAATTAATAAATAAATATATAATTAAATTAAATAAATAAATAAATTAA 73416
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                                                                                                                                                                                                                                                        410 AAAGGAAATAACAAAAGTTATTAGCGATAACCTGCGTAAGGTGTCAACAAAATATTTT 469
                                                                                                                                                                                                                                                                                                                                                             530 ATAGGAAATCCCTCTCACAGTGAACTGAATTATCCATCTGAATTATCAGTCCACTAATTC 589
                                                                                                                                                                                                                                                                                                                                                                                                               590 CATCAATAAAATAGATTAGTGTATTGTTCTCTTCAGTACAATTACTACCATTAIGCAAIG 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   768 AAATATTTGAAAAACACATAACACTTTGAGTATGATAATATCAACTATTGACTTGTTTT 827
                                                                                                  230 GATAAACTIGCCATAATAAAAACTCTITGAAACATACGATATGTTATTCTTTTCATAACT 289
                                                                                                                                                                                                                                                                                                           110 TAAAAAGTACGTTGTTGTTCTCCTCGTCTCGTCTAATTTCTGTTGACGAGGATTAATAAC 169
                                                 170 AAGAAATACAGGAAACCCTCCAAAAAAATTTTGGACCTTACACGCACATAAATTGCG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      828 GAAAGTAAAGAATCAAATTTTTTTTTTTAACTCGACTAATGCACTTTACATCAACTGGATGT
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                                                                                                                                        1364 GGTCAAAATAACCGGCTATTTTCAATTTCCATTCAACTTGTTTTCTCAACAATATCAAAA 1423
1184 AIGACIACATITIGITICACITITIGIGGGACITITAAIACCGITITITGCAACITCTCTI 1243
                                                                                            IGTAICACCIGIAICCGCCITITITAACAIAGCAACTCTIGIAAAGICCCTTICTTITCC 1303
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Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 169946)
Hyman, R.W., Fung, E.L., Qin, F., Rowley, D., Mao, J., Tamaki, T., Kurdi, O.B., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Aug 12, 2000 this sequence version replaced gi:8810447.
* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
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Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W.
Direct Submission
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23467 23666: gap of unknown length
23667 169546: contig of 145880 bp in length.
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85181 TAAATTAATAATATTAAATAAATAATAATAAATAATAAATAAACAATTAAATAAAATAAA 85240 946 CAAGTCATCTATAATTCTTTGGATCCAAAAACAAGGAATTCGGAAATTCTGACGATAAAT 1005 1006 GTCGACTCACAATTCATTGTAAAAGGGAGAGTTTTGGTAGGCTCATAATCGCTTATAAT 1065 110 TAAAAAGTACGTIGTIGTIGTCCTCGTCTCAATTTCTGTTGACGAGGATTAATAAC 169 1184 AIGACTACATTITGTTTCACTTTTTGTTGCGACTTTAATACCGTTTTTGCAACTTCTCTT 1243 170 AAGAAATACAGGAAACCCTCCAAAAAAATTTTGGACCTTACACGCACATAAATTGCG 229 530 ATAGGAAATCCCTCTCACAGTGAACTGAATTATCCATCTGAATTATCAGTCCACTAATTC 589 710 ATAITITICIIGICCTICITIGITITITITICIAACAAA--AIGIICCAGAAITITITAAA 767 888 TATTIGCAICTACTACT--ATAAGCTCAAACAAATTATCITICAAAAATGITATAATTAA 945 230 GATAAACTIGCCATAATAAAAACTCTTIGAAACATACGATAIGTTATTCTTTTCATAACT 590 CATCAATAAAATAGATTAGTGTATTGTTCTTTCAGTACAATTACTACCATTATGCAATG 350 TAAGAGTTGCCTAACCATTGAAAATAATAGGCTAAGGTTTTTCCTGATGCGTTTAACTAA 410 AAAGGAAATAACAAAAGTTATTAGCGATAACCTGCGTAAGGTGTCAACAAAATATTTT 650 CIAGCITATIGITCATAATTAGCCATGITGCACACCCTAATTCGAACAITAACTGTAICC 768 AAATATTIGAAAAAACACATAACACTTIGAGTATGATAATAICAACTAITGACTIGITTT 828 GAAAGTAAAGAATCAAATTTTTTTTTTAACTCGACTAATGCACTTTACATCAACTGGATGT q δλ Op Вb Db ò g q Op ò ò δy Pp Dp ŏ ŏ δŏ ŏ g ö Op ò q δλ QQ ά qq Óλ q Op g δ δλ g Óλ ŏ

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Dictyostellum discoldeum chromosome 2 map 4603055-4707067 strain AX4, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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1 (bases 1 to 104014)
Gloeckner,G., Eichinger.L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K.,
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
1364 GGTCAAAATAACCGGCTATTTTCAATTTCCATTCAACTTGTTTTCTCAACAATATCAAAC 1423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence and Analysis of Chromosome 2 of Dictyostelium Unpublished
The Dictyostelium Genome Sequencing Consortium
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Funding
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* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
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                             644 GCAATGCTAGCTTATTGTTCATAATTAGCCATGTTGCACACCCTAATTCGAACATTAACT 703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.

[ (bases 1 to 14867)
Gardner, M.J., Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, L.,
Koonin, E.V., Shallom, S., Mason, T., Yu, K., Fuji, C., Pederson, J.,
Shan, K., Jing, J., Aston, C., Lai, Z., Schwartz, D.C., Pertea, M.,
Salzberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O.,
Smith, H.O., Fraser, C.M., Adams, M.D., Venter, J.C. and Hoffman, S.L.
Chromosome 2 sequence of the human malaria parasite Plasmodium
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GLKKGSLKSKTRKSTSGSKFKPLNKYFLSKIKIVTSLNKIPSPLKEQKNTEVNLPESL
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Plassmodium falciparum chromosome 2, section 35 of 73 of the
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Gardner,M.J.
Direct Submission
Submitted (02-NOV-1998) The Institute for Genomic Research, 9712
Medical Center Drive, Rockville, MD 20814, USA
Location/Qualifiers
1353 CTATAAATAACGGTCAAAATAACCGGCTATTTTCAATTTCCATTCAACTTGTTTTTTCAA 1412
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RY IKHLHEEDNFDQKDQYVCSLFFLNNLFFDK I HFHY IYNLMCHVYKTYNYFKCNKL. INEDI I SLLLLFCSKFQYF I ENNSNDRYCRKELJHLKYN I I DDL I KNYLNTYKS I SI D NI SKIFI SLSNSKYTCEVNENLLLESLQSEFEKVTKTSKKGG I HAMDNNLLDNNNSCE KKILYTANNLYMYEMYCYVCEMLERVLSSHKEQNLFSYNYNKNVEHKMFDKILCHISE DDYIEMSNTWYVLFYDYLKNINSERQSNILRNNSTNDRFIDEIKEKKYKLNNNTLIKH NNVKLNYEMSKNNSNGNISHLKDDKNKNHNNVEMDLIDNKNBNKKIQEKGQNGENCEN CKDVLVNILINIFGELKMEKKFLFFQLYMYLCNITKFRRRYVSSSSLFHMDVFKIIK DMNLKYLCLEMYKIREECAFLYTIDIYLFKER" 1019 c 1106 g 6458 t IFYKMENYKDFHFKLKDSDLLSIKLLSNTFVKINEVYNSYDFYLLFNNISCÍLYNFLV NRNSVKKYKDTYIYILNDLSFVYKYIKNNDRTKKKKNFFLLSSSMKELJCKNILSVSN KYEHRYIEYKKENLFINLNKIIECLIKLNIFLYLKKKKTYLYLYKQSLCPINLKENIL HEIYKLLFIFNKYLNNNSNIPFNKNLIQEMEFNLYYFREIKNEKNYIIKMNKKEIYKK CFAKFHENVDHIDNEKILNILRLYVDNSILDIDINNKMLCNLNNNLINENIEYISKLL NFYCTLIKKGKYDNDMTIYKLKEVIKATHHILCDKTKNLETFCSDIDYSTLLNSLNNK FILNKIIDKNFILFYECLLKILLNIKFVNFQSLCISLISLKNIYYNILRNNVYIVNNV LFNDIMKFSLYLCNIFLGKRIKTENENAVLIIHNNDQTNYSNKENIKDIIIQKRIKEY

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13; Gaps 0; Mismatches 731; Indels Conservative Matches 565;

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a

284 δλ q

Qγ

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RESULT 10

523 TATTTTGCACGTTAGCTCTATAGAAAATATACAAACTAAATCCTTAAGGAATTTCCTCTA 464 δ

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Dp

584 TAATTCCATCAATAAAATAGATTAGTGTATTGTTCTCTTCAGTACAATTACTACCATTAT qq δŻ

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δy

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8316 QQ

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879 ACTGGATGTTATTTGCATCTACTACTATAAGC -- TCAAACAAATTATCTTTCAAAAATGT 936 = = = = = =

1171 TTGCCTTATTTTTATGACTACATTTTGTTTCACTTTTTGTTGCGACTTTAATACCGTTTT 1230 1351 AACTATAAATAACGGTCAAAATAACCGGCTATTTTCAATTTCCATTCAACTTGTTTTTT 1410 ACGATAAATGTCGACTCACAATTCATTGTAAAAGGGAGAGTTTTGGTA-----GGCTC 1050 AAAGTTAATATAATTAATTTATTATTATAAATAAATAATTGCTTTAATTCATTAATT 8615 1231 IGCAACTTCTTTTTATATCACCTGTATCCGCCTTTTTTAACATAGCAACTCTTGTAAAGT 1290 1291 CCCTTTCCTTTTCCCACTATTTTATCATTCTTGAAATATGTAATCAGAATAGTTTTTCAAA 1350 937 TATAATTAACAAGTCATCTATAATTCTTTGGATCCAAAAACAAGGAATTCGGAAATTCTG 996 1411 AACAATATCAAACACAACAGGAATCTCCTATAGTCACTCGCTTTTAGTT 1459 8556 9618 1051 8736 g qq a g δ ò δ g ŏ QΥ g Q δ g δ g

PFWAL3P6 library MAL3P6, complete sequence.
298551 AL010161 AL010170 AL010212 AL010213 AL022222 AL139179 298553 298551. d G1:3758836
HTG; 40S Ribosomal protein S11; 40S Ribosomal protein S11; 40S Ribosomal protein S11; 40S Ribosomal protein S15A; band 7-related protein; CDC2-related protein kinase; DNA-directed RNA polymerase II; FN transporter family; kinesin-related protein; PVP APPase ring finger protein; PDZ domain; proteasome component CG; putative cleavage and polyadenylation specificity factor protein; putative inorganic pyrophosphatese; triosephophate isomerase; trophozoite stage antigen; ubiquitin-conjugating enzyme; zinc-finger protein. Plasmodium falciparum 3D7. Plasmodium falciparum 3D7. DEFINITION ORGANISM ACCESSION VERSION REFERENCE PFMAL3P6

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 16439)

Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T.,

Churcher, C. M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T.,

Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S.,

Mornsby, T., Horrocks, P., Jagels, K., Jassall, B., Kyes, S., McLean, J.,

Moule, S., Mungall, K., Murphy, L., Oliver, K., Quail, M.A.,

Rajandream, M.-A., Rutter, S., Skelton, J., Squares, R., Squares, S.,

Sulston, J.E., Whitehead, S., Woodward, J.R., Newbold, C. and The complete nucleotide sequence of chromosome 3 of Plasmodium Barrell, B.G.

Nature 400 (6744), 532-538 (1999) 99376085 falciparum 10448855 MEDLINE PUBMED JOURNAL

Murphy, L., Bowman, S., Harris, D., Lawson, D., Quail, M. and Barrell, B. Unpublished (bases 1 to 164399) JOURNAL REFERENCE AUTHORS

us-09-725-010-1.rge

TITLE

COMMENT

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Lawson,D., Bowman,S. and Barrell,B.
Direct Sibnission
Submitted (14-406-1997) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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TKYDIYDNPTLQKVPLLYHKRE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MTTFDIYNKRLKKEKPCFKLKRDSPLSFQKCIEIWCDIELIKYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGDDTYYSLLKRYYGEKKKNKIKYGNVGNYDNNSNHSDDNNKNHCNDNNNKNHCDDNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNNHCNDNNNNHCDDNNNNKNHYVDNNNNKNHYVDNNNNNNHCGVYFKRKRKEKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNISYHNIVKDFFLDVCKYSKDYEKEKLYFMSKLYTCMIYCCYILIKNKYYLDFFCLY
LLLKSYFFIDTIINKYIVLPNFTCHKKFLRLLFLLCNICNYKDTGENYNIYNEERIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="PFC0700c (MAL3P6.1), hypothetical protein, len: 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MNTKLFFGNSLCNKILYKNVINNLRGCYNIAGPFIISYLKLEYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IHDEKLLKKLRYEIKEIIYSNILYKTKKNFQLFHMFYNYKYNYNVEYVTRQYMFNLSM
                                                                                                                                                                                                                                                                                 For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(4080. .7204,7332. .11478))
/gene="PFC07055, MAL3P6_2"
complement(join(4080. .7204,7332. .11478))
/gene="PFC07055, MAL3P6_2"
/note="PFC07055, MAL3P6_2"
/note="PFC07055 (MAL3P6.2), hypothetical protein, len: 2423 aa, predicted using hexExon but revised: changed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="PFC070lw, hypothetical protein, len: 298 aa, revised: new gene prediction"
                                                                                                                                                                                     On or before May 14, 2001 this sequence version replaced gi:2665320, gi:2982570, gi:2982576, gi:2894503, gi:2982580, gi:2894373, gi:2982530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(156..161)
/gene="PFC0700c, MAL3P6.1"
/note="potential splice donor sequence at 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein, PFC0705c"
/protein_id="caB11149.2"
/db_xref="G1:7768285"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /produc_t-"hypothetical protein, PFC0700c"
/protein_id="CABI1150.1"
/db_xref="GI:3758865"
/db_xref="SPTREMBL:077394"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein, PFC0701w"
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Plasmodium falciparum 3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  splice donor sequence for exon 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFC0700c may indicate splicing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predicted using hexExon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(152. .1075)
/gene="PFC0700c, MAL3P6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SPTREMBL:077393"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="PFC0700c, MAL3P6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAB90508.1"
/db_xref="G1:7768284"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:36329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .1075)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2866. .3762
/gene="PFC0701w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2866. .3762
/gene="PFC0701w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="MAL3P6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="3D7"
3 (bases 1 to 164399)
                                                                                                                                                                                                                                                                                                                                                                                    .164399
                                                                                                                                                           CB10 1SA, UK
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REFERENCE
                                 AUTHORS
                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
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KTCVWENSLEFY PROBELLNY IY IY NILFVWIQKKHLTKLCKFLFLKMIKPFLHFLFT
YVYMCINKDY SFEY I INTNEYAHFPE I FHNORK YVDPKYLLGDVCI SLPVFLNYSMDV
THY TALLSSILRVANBEN FFE SI PKKOS RENEKCYOPY VDKTNSMISI ITSRYNY NEN
VDI LNILFYT SMDK IT TSFLOLY NSPOYK GRKUNKY ENVET KYWNDEKECEVAYEKI
KLDINKKLEKDLLIFY NMLSNHVNGMCLY DKRAMENY FEEKK KIDPKKNY VDKIYEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           len: 380 aa, Similarity to inorganic pyrophosphatases eg celegans (TR:018680) BLAST Score: 431, sum P(1) = 9.2e-41; 43% identity in 201 aa overlap, predicted using hexExon, pfam: match to PF00719 Pyrophosphatase, Inorganic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HNSIYWNYGALPQTYEYPKHIYQNKSKKNKEALLFTGDNDPLDILDIGSACLKIGQVV
VPYLLGAFTLIDGGELDWITAINKEBKHYBDINSLSDIEXYYPHTLSLLLEWPRSYK
WADDTKLINISKQIYDKKESBILIKKTHYYLLEFREDVKKIKEEHSETIKEHDYVNA
ONIQPNYDKLNNINDEDMENNLLEDINITYYKSDSAYKPDLNIWTP"
                                                                                                                                                                                                                                                                                            DEFOKKDYKNGLEKKYGYPSGNSKKRNHHKKEIIHSYKCKKKKKKKKSECIYISKD
IICINSELAIWLKKRNRKLCLYFKPLQNYFCSHYONYLHTHWYFSKIGFIRSYIKI
FILDTRIELAIWLKKRNRKKLCLYFRSDSVINLTYEKKYKEKNKMKGNYKNTYDFNI
PLGELFVYTINCIKKTLIYENKIRNIINDKNYKNPLHIYLKIKKGECIEFLNFLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRKEKNIKKNRININYSYNNKEYILKDLRRCOKKIKKNNKIIIKINNKCMYNMNNIY
SRILGNELNRUKKRRNKLESSYNILMDCLHFFIRKHIKNNFTYNNGONKIVODIK
ELYSLSSYNNINDAPOGRAKREMKKFDIIIDHKEKLINGFNFVOVDIISLGLHNN
NNNKALENKGKSGFYRPYGSNKNINNININKNININFNKNININKNININKNNINKN
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DNFVPISPWHHIDLKNDDGTYNMIVEITKYNYIKLEIQLREKFNVIKQDKKKGKLRYY
                                                                                   NIKKKNKFHDFIFNNNNYCYYNKMLSFHKNDIYNDDDDFIKNVLYIHYPPTKNMNDIF
TSSYNNIITKKKKIGNNQIIKNKNIYMNKNIVWNKNIVKNKNVYKNKNVYKNNKIGKN
                                                                                                                                                                 NKIGKNNKTIRNTFNOFLISPFKKSENFIWKKSFVNDTNVLKILENNIIHTKKEKYKN
VFLTIINSMYVSIHANIINSLNNRIDEYRFVIFNRFSNICNLKKYIYNKENVHTNKDY
NIWKIDILNCLLGYGGNIFMSGRNAHTFKRNNEKKGBKRYMYKKKKKNVKAVESIKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CY INYKVRRMFFKERI NFYKSIDNDISFSSSFNNNICTKNKMIRDYNNLSNI IYGLSP
YKHNNNNNDMLYKNI NLCLKEKNEFKKVLNDDNGVIYNKETY IHELNKKEQENFLRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNINQNINKNINININININDKGSNMNNPCNHQNKNREDIHYNNHYKHMIYFHNKHDK
SELLKKNSGGLEYNHEERKYKEKIYSCKRNFEIENINYFIYRNIYRPIKYPJITNKI
LINSFLINMNLLIYFYLLKCILFDDMDDNYNFLCNILFNKRNKIINKIENDDYNDNCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHIFVNKNKHMVQYFLNKNFYTSCNIKNKCVDKNKLYYTDISTIFFYIHFKINVPKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIFFDHKVVNYYNDIYRLTSLLYFSLLNLNYIFLIFSTLCRPTIFQCKKWKGGNPSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGONKIVOKNNMATLKNNKLKIYKEKKNINFIKNDSYKDDYKNDDEYDYHSSNSTLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTFFQKIVTVHNFYDLIKIHESFVQHIFKLSFLSKTDLSFIKIIFNINTVNIFKYIM
KSIIPLGGNIKQLNVSKTCNINTYDEHTLLNYEECKQHDYYKSFLFLFEQNFKILEHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MGSKLINVEGGNNQDDNKYNSNNVISINNKVNKNDYFIETNKEL
EHHTINNILVYNYHQSMYSQNMLNIPNSYFNEYENKLKEDTLNNLNTLFSPLTSIQNN
                                                NNNNNKYKY I HPNYNLYGNHVNNLFVDTKKMKS I FLLNHKETGNPFSLNNRFAQDTSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENLVTNQIFKEKDFKYMHIINNIKDNHLLENEDYINSCPCYITKNTSNVYFMTKEKYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVGFHKNFIHFKKLNKFLQNIKIYNDTLNDLYKIRSEMHFIINALYDYLMYMNLSKNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IILLTSQRTQDFIKQFYINRNHFIQYVNKFKNSDLSYIYQKFFFNEYYAHLCDESYDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein, len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="PFC0710w (MAL3P6.3), Inorganic pyrophosphatase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(7326. .7331)
/gene="PFC0705c, MAL3P6.2"
/note="revised splice donor sequence cag/gtgcaa for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Match to PF00719 Pyrophosphatase, Inorganic pyrophosphatase Score 91.89"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(14251. .14913,15153. .15215,15458. .15874)
/gene="PPCO710wMAL3P6.3"
join(14251. .14913,15153. .15215,15458. .15874)
/gene="PPCO710wMAL3P6.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(14620. .14913,15153. .15215,15458. .15652)
/gene="PFC0710wMAL3P6.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"putative inorganic pyrophosphatase"
/protein_id="CAB11148.1"
/db_xref="C1:3758863"
/db_xref="Swiss-PROT:077392"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="PFC0715c, MAL3P6.4"
complement(16357. .19383)
/gene="PFC0715c, MAL3P6.4"
/note="PFC0715c (MAL3P6.4),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pyrophosphatase Score 91.89"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(16357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFC0705c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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1008 aa, predicted using hexExon"

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DNYTNKEMINKLSDDKKDALKKNSAEVEESSKNNYTKNVLLNNSQNYSIANLKDEQI
VENENVENVENVENVENVENVENVENVENVENTESETERR
KELIKSDELLKKLENEMKYDENVENVENTESEPERR
KELIKSDELLKKLENEMKYDENLYMKOLYPOLSEHHKRENSENTENTERENKENSENKC
SRGYTDNIKKKQSMGOYDIGRKIEGRYTYYTHYENNEYSFSLYFFLRPYIKKHLIDI
DNNFFSLTINKHNIIKDIFNHPINSSDSIWSLTDNEDNHFMENEMNEMQFPVYDITNI
                                                                                                                                          /translation="MATLYIFIGIIVIILCSRFCNNVNENNIGKSHYPIFLKBRENRN
NNFCSNVYNNIGRKKIKKNKNVYPHSLGYIFLPLYNKLSRSNTNNNVSRNKCLVDYVP
NKKKQGGNIFLFHNVHVINKMKFQKNVSICAESKKRNKKRNKKRVHHYFMDKNLGDI
                                                                                                                                                                                                                                          FESNÄTEGIIDKNKSSNVINNDSEŽNHPNIHNNEGTYNNIDENNPMYEGMPNHLSDSN
LESAMKKABEYIKGKEDDIIERREKEKKKKIVEKMKDDEDVFTDKLLDLRIYDMLKYY
YRNNIYRTSHELVNNICMMMKSTYSNYVDTNKEIQRREKKKQEEEKKDEEKNKKKEE
                                                                                                                                                                                                                                                                                                                                      LINISDNEKDTKHNETNINYKRVNVNDKDVNHEDIIKGKKAKEKTDDEIGSEIIEKD
ISTAN'SKDRAVQYLANFSFDKNNEKLNSEMESLKLYNKKNLSKYFFSLYKGNIILKQLY
ISTAN'SKDRAVQYLANFSFDKNNEKLNSEMESLKLYNKKNLSKYFFSLYKGNIILKQLY
YEGEDLQDRAKD STERKKKDDYRKYDSHNYDSNRYDNNYDSNNILENNYDDKY
VKDTLSQNLFELYDERY IDKREYMKSVYTIENIYDTYSDNYJLNNKKTNIEFPL
IDSHHIIQKCLLTMKKLEKA FFY IKNNLLFHSFTSNDNPINKDDRNYDVIINEEPTL
MELYLCNIYGINEKWMGIIPNMFENEHKTNMFLKNYSMDNPONNMITLGDPSNSTKGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 145318 ATAICCAAGICTAATAIGAAGIAATGAIACACAIATAIGICITITITATATAACACGCA 145377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145438 CACCATTATGTAGATAATACTCATGTGGATGGCTTCTTAATTGGAAAGGCTTCATTAAAT 145497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 145498 GAACACTITAICGATAITATAAGATAIGTAGATC--ATIAGCATAITTICCCTGTGAATA 145555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 ITTICCIGAIGCGITTAACTAAAAGGAAATAACAAAAGTTATTAGCGATAACCIGCGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328 AAAAAAAAAGGAAATGAAAAGGTAAGAGTTGCCTAACCATTGAAAATAATAGGCTAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.0%; Score 73.4; DB 3; Length 164399; 42.9%; Pred. No. 0.0051;
                       /product="hypothetical protein, PFC0715c"
/protein_id="CAB11147.1"
/db_xref="G1:3758862"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.0051;
0; Mismatches 621; Indels
                                                                                                                         /db_xref="SPTREMBL:077391"
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Matches 470; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T., Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T., Cherles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S., Hornsby, T., Horrocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J., Moule, S., Murphy, L., Oliver, K., Quail, M.A., Rajandream, M.-A., Rutter, S., Skelton, J., Squares, R., Squares, S., Sulston, J.E., Whitehead, S., Woodward, J.R., Newbold, C. and
145916 AAAAAAAAAATATTAATTAAGGAAATTAATTAAAAAGAAATTAATTGATAAAAAGTTGG 145975
                                                                                                                                                                                      Db 146036 CATACATATTTGTGCTTGGTTTAACAAACAGTTACATTTTAATAATTTTAATTTTTTC 146095
                                                                                                                                                                                                                                                                                                                                                                           988 GAAATTCTGACGATAAATGTCGACTCACAATTCATTGTAAAAAGGGAGAGTTTTGGTAGG 1047
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                                                                                                                                                                                                                                    TITITGCCTIA--TITITATGACTACATTITGTTTCACTTTTTGTTGCGACTTTAATACC 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                1226 GITITIGCAACTICICITIGTATCACCTGTATCGGCCTTTTTTAACATAGCAACTCTIGT 1285
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                                                                                                                                         1048 CTCATAATCGCTTATAATGTACCTCTAAAGTAATCTAAAACAAAAAACACATTTCTAAAA 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The complete nucleotide sequence of chromosome 3 of Plasmodium
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Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 113880)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 113880)
Hamlin,N., Bowman,S., Churcher,C., Lawson,D., Quail,M. and
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Lawson,D., Bowman,S. and Barrell,B.
Direct Submission
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AL008970.3 GI:7672212
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may suggest splicing"

complement(7161...13970)

dynea="PFC0440c, MAL3P4.25"

complement(7161...13970)

/genea="PFC0440c, MAL3P4.25"

/note="PFC0440c (MAL3P4.25"), putative helicase, len: 2270

/mote="PFC0440c (MAL3P4.25"), putative helicase, len: 2270

(WP:F22B5.3) BLAST Score: 290, sum P(4) = 5.9e-31; 34% in 199 aa overlap, predicted using hexExon, contains match to PF00271 halicase_C, Helicases conserved C-terminal domain
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IEKNDYTFINGETGSGKSTCVPKFLLEENIRENKKINIIVTEPRRIACIALSKILSEL
TNEKLGQKIGYRISGESLYDSEKTVITYITIGYLFKLFLHHKNNYKKFTHVIIDEIHD
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/translation="MNNTFKINKKRRTVYESYNIINIANKKRYMCNDNKMDNDNNIIN
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SNESHWATQDGHPIYNHNNNNDGRIKNRKDISLSSYGYNKISNDNLSKENTSYINQY
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HENLYTHKNILLGIKTSINTEEERIPHIKNTYDNKENTQIIENTFNYDNKLKEKNTFG
FYNNSLLQNALENDNIDLDIIYMSDKESQKYDNLYFNSKVTSKEGLCEKLKHMIYYYY
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NEALFLQNFPKKTLFLYSYLKDTFAKTIQTLKKYDYVPKYCQGGILSKKHKNNDSDDD
HDHHVGNKQNNDSTNHQDIEKNQVNVINNNNNNNKAKSIPIYLGRRYSYNTFSTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKSSVPTNNIDKNEDTTKYVIKANEKIYNRAQESGKYKQLFDINKFFKKEIEGHPYFQ
KIKKKNEKAKKEKEKEMAQLKKQKDYTNNYFHTSNAQGNFNQQKAGNYQNQENEENDFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLEKOKLNKIKDKNNNNNNNNSKFSKDGDNEDFNNKNDLYNPSDKLYNNNDDIDVHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKNFLFPSLNSGIILDITLLKNIYEVSNILLSNNEKDQSIHIDYIYEVTKYIKENLRV
RLTHSENVCLNEEQNIHLLDNDPNNFEIYKYYQVLNLFKDYNKNTEEKQYEKIGHENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEYEYDYLTGGAGILINDETAKRIYECKECTCPSTNSSMDDMIFGKWAKELGILAINF
BGYEQNSPLDYNKKYINTLVPITYHRLNKNRTTKESRDMYFNYLVNYNRNDKEQNKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u> QGDKNVNDDENVNDDENVKGDENVKGDENVKGDEYMKGDENVKGDENVKDDENVKDDE</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DQRPETEEDAINPMDYEEYMENLSNFEDDGEPYDEYDDYDDFVNTINADKLKINDQNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLEEIITKEKRFFLNDDDDNDSNDKYILKTDEVNKYKGFFIGYGFNDDIPSVIHHYNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHEETSSEGNENLNRNTKHNNDNNNDNNNYSEDAIAELLLSYFNVFYPISTCMCYSIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YVDYLDRNHKNMIDNVFHYFFYVNMYDEKNKVVTKIEHNADMNSKKNKSKNPQKLNNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIKGDDNNYNVDNMENIDDIINMVESVDDDVMERNKKGTGKEKKDDKNHNNKEKATDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MKVGIIFFCLFFFVVLGACNNVKERIFKNIKKRTKFIILNEPIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESFSENLFHTLLFDLDVDKNLYTLDESLENLENENYSSIFRLYVDTYKNIKENEDDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNIRYIFLGTSFSRIHPLNFEYFLRKLNKYIYNGNIYEKGNVDIRGILEEYNKEIEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      may suggest splicing"
complement(7159. 7164)
/note="potential splice donor sequence at end of PFC0440c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6245. 6250
/note="potential splice donor sequence at end of PFC0435w
                                                                                                                                                                                /note="sequence duplicated in MAL3P3 to include complete
                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein, len:
                                                                                                       'note="original nominal overlap with MAL3P3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"hypothetical protein, PFC0435w"

'protein_id="CAR15616.1"

/db_xref="GI:3764023"

/db_xref-"SPTREMBL:077361"
                                                                                                                                                                                                                                                                                                                                                                                        /note="PFC0435w (MAL3P4.26), Hypot
1294 aa, predicted using hexExon"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLYEQIKDIAQPPVNFQNDQNSNTFDFDTDEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative helicase"
/protein_id="CAA15615.1"
/db_xref="GI:3764022"
                                                                                                                                                                                                                                                                                                                                  2364. .6248
/gene="PFC0435w, MAL3P4.26"
                                                                                                                                                                                                                                                                                            /gene="PFC0435w, MAL3P4.26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                          /clone="MAL3P4"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25.70'
                                                                                                                                                                                                                                                                 .6248
                                                                                                                                                     . 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
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                                                                                misc_feature
                                                                                                                                                         misc_feature
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gene

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/translation="MOINNIMEEVOAIKVLPHMMFNASKLKVLSDYVNVAFENNEYYD
NDVMLTLLRLECLYPHCYDKDIIKKILICVLYNINNVDMNMYMSLINSSLYDDNIKSY
NYMLTLLRLECLYPHCYDKDIIKKILICVLYNINNVDMNMYMSLINSSLYDDNIKSY
IYYYELIKNOOYKKLMNCINNNIGNEYNNCDYSYLKRNDKNFICNIRKYILNTISISFE
SIYTKNMSETUNIONTOLEOFLNENKWTIKMINHKGKDEQICYNGNIETVQNKKNIN
TYFTEDNIGSYTTKLNH"
complement(16668 . 16677)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human
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                                                                                                                                                                                                                                                                                                                                                                                                                                    NUNDNOSGETI NADGITPNNTHMNEINGMNYFNVYTKYCLFDYSNOMIYLKFLFSLSF
TPLFIHGSPNLPLRDLNEGKKKSKKLMNVLNFMIDNKLDVKNCIYFSGVYIPDINILK
RAICIMCPYLSFDIYVSKNIYYYYFHNNYHNYHNWINDDDSYYNKTIODKGDAD
MSONSYLLNITOGGHDTDGITSGVSPLMNNNMYGNNYIHNNVYYPCNGINNYNNNV
VNSQNNYMMKJMSNYYSESFLMLTSGKNYPDIIEKIRNKLLYKYNNNVEKSIFNNFY
NNILNLLQOPVALIYPVYSNKYDEINNASICTNIINMFSNGKWIFTMPLFNPNKRKCEV
SEYFNHKYELKKPKRHLFLNYMWFLNTDNYKIKKNKOKEHVMOTNNALNNNNSLGKNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNDIHENNINDYSLUDQEDQQYNKGYYDDYDDYDDYDDDNUDDNUDNNNNNNDDDN
NNDDDYLSWNYVESDNNYHDNNPDCOYEGNDSSANGSDNNKGSKQKKMKCNLNFRSY
LGFLSMCPFNEDTRANIYDDNADDJYAVCSSIDYSYTNDTYTWYVYTLPNKYFLTF
FLSSIPYHDNVIIQTRTNLYTSDILSIKIFDSKEIILKNMKKMKHKKHTTNYYYDTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INKDGPNNDNRVDANDKNVNNONDKNVNDNDKRVNNSQONGGNOKDHFDDEDEEYFSDED
IMSOTEENNIIKENLYIKQIVINMIEENNMDYINYNKYSMDNMDIDEHFNLQYLYEDE
HFINLNEKWYNNKGEILMNTYDYLXNSLKNENDYNQYNNNNNNNNNNNNNSSYWYKNI
                                                                                                                                                                                                                                                                                        SHAENKKLTIYDVLSMIIEKPSKEKIKSTRVELEKVKAVIKIKDKLVISIIGQIMIRF
NLSINLCRLLLYGVLLDVTFDTIILIGILNTNDIFPNINLYSSKNIYSYAVSLEICSK
OKAYFDGNIYSEPIMLRNVFLEWLCVYLLXVQGLKKENKFHRKELKYYYMNTCSIMNK
RNHYNSKKLLCVINSVDNLCKKMLKMLNKNSNAYKSCYYLLYLLRGGSDINYNMGNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEKALNSLEAVKSSYLNNNFSVQVQNTMNAYERTNSEDFLFFQPINISPIKEANYKLR
                                                                                                                                                                                                                   KNIEYNDKKKAHILVKKWINKSSMEORKGRCGRTCHGICIRMISKNFLNLLRDHKISË
IYTHSLHLLYLYILKSMSVLNGLINKRNEVVHCDNTNVYNVKEVKDQKNGICKNEISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STINNPNITKHDLLRVNYLRYVMSKLLLSLTESFNRQEIEQNTQPLKLSEKSKRKSVI
RSILLDIVLLFIKLYLHNKQKDEQMFKLIIMSATMQSNLFYSYFEHPNIKMGSIFIGT
KIFSIDTFYIEDIINYTRYGSRNIHDEKINDEKINDEKINDEKINDEKINDEKKINDONKKSCD
                                                                                                             FNNNNNKYCNDKNKDLDVDEIIPANVFSNISNLCLELVYNLCLKGDSVIIFLSGMQDI
                                                                                                                                            TDMYHQLSMIINNNMDNPSNSNININNGNDANDANDVNNMHNMHNMHNIANQLTY
                                                                                                                                                                                     HRTDIKIHIHMLHSCLYDNTIHKLKHNDTDINIFLSSNIAESSITIPNVRLVIDFCIQ
                                                                           DKKSCDDKKSCDGNNNFVKESVIDFILRRKNCNKINLSKNSEMLLYKIKSEYDKNIHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein, len: 145 aa, revised: extended upstream and added exon, GC plots suggest more, similarity: eg to hum cDNA AAF29135 HSPC172 (219 aa), fasta scores, opt: 257, E(): 6.9e-11 (40.0% identity in 115 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="predicted splice acceptor sequence for exon 2 of \ensuremath{\mathsf{PFC0A41c}}^{-1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="PFC0440c, MAL3P4.25"
/note="Match to PF00271 helicase_C, Helicases conserved
C-terminal domain Score 25.70"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="predicted splice donor sequence for exon 1 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(18192. .18242,18754. .19140)
/gene="PFC0445w, MAL3P4.24"
join(18192. .18242,18754. .19140)
/note="PFC0445w, MAL3P4.24"
/note="PFC0445w (MAL3P4.24), conserved hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /_ote="PFC0441c, hypothetical protein, len: 235 aa, revised: new gene prediction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="variable sequence, 9 or 10 Ts" complement(join(16039. .16667,16813. .16891)) /gene="PFC0441c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(16039. .16667,16813. .16891))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein, PFC0445w"
/protein_id="CAA15613.2"
/db_xref="GI:7672214"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein, PFC0441c"
/protein_id="CAB89483.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="SPTREMBL:077358"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(16807. .16812)
/gene="PFC0441c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(10956. .11255)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMYYNEVAPTLDKFRRTNRQV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="G1:7672213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="PFC0441c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="PFC0441c'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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EKINVYSLYEKTNIFQSLEKKGIETIEGDGFKIQCYDTLTGIKIFIVHKDDLNIEMN
TYLKRVYELYSDIILKNPFYDIDMPIRSAVFNEQIEKLFSNIS"
                                                                                  /gene="PFC0450w, MAL3P4.23"
/note="PFC0450w (MAL3P4.24), Hypothetical protein, len:
/109 aa, contains possible signal sequence, predicted using
hexbxon"
                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                            52613 ATTCAAAAATATTTGTATTTTATATTTTTAATTATTTAATATTTTATTTACGGTAGAA 52672
                                                                                                                                                                                                                                                                                                                                                                                                                                         52556 AACAAATGGTAACAACAATATTAACCAAACGAATTTTTAAGAATAAATTTATT---ATTT 52612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52973 TCTTTCTTAAAATTTAAGATTTAAAATATATAAAATATAAAAAATAAAAATGAATAAATGA 53032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GITTAACTAAAAAGGAAATAACAAAAGTTATTAGCGATAACCTGCGTAAGGTGTCAACAA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460 AATATTTTGCACGTTAGCTCTATAGAAATATACAAACTAAATCCTTAAGGAATTTCC 519
                                                                                                                                                                                                                                                                                                                                   220 ATAAATTGCGGATAAAACTTGCCATAATAAAAACTCTTTGAAACATACGATATGTTATTCT 279
                                                                                                                                                                                                                                                                                                                                                                                                        340 AATGAAAAGGTAAGAGTTGCCTAACCATTGAAAATAATAGGCTAAGGTTTTTCCTGATGC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTATATATAGGAAATCCCTCTCACAGTGAACTGAATTATCCATCTGAATTATCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            580 CCACTAATTCCATCAATAAAATAGATTAGTGTATTGTTCTTTCAGTACAATTACTACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTATGCAATGCTAGCTTATTGTTCATAATTAGCCATGTTGCACACCCTAATTCGAACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITITAAAAAATATTTGAAAAAAAACACATAAACACTTTGAGTATGATAATATCAACTATTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            820 CTTGTTTTGAAAGTAAAGAATCAAATTTTTTTTTTAACTCGACTAATGCACTTTACATCAA
                                                                                                                                                                                                                                                               Length 113880;
                                                                                                                                                       /codon_start=1
/product="hypothetical protein, PFC0450w"
/pprotein_id="CAA15614.1"
/db_xref="GI:3764021"
/db_xref="SPTREMBL:077359"
                                                                                                                                                                                                                                                             5.0%; Score 72.8; DB 3; I
4.6%; Pred. No. 0.0069;
ve 0; Mismatches 407;
                                  19528. .19857
/gene="PFC0450w, MAL3P4.23"
19528. .19857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   940 AATTAACAAGTCATCTATAA 959
                                                                                                                                                                                                                                                                                 44.68;
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                 Best Local
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                 PAT 06-JUL-2002
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/note="lower strand of DNA sequence 25; after bisulphite treatment and P CR"
1 0 c 97 q 979 t
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                   linear
                                                                                                                                                                    Method for the detection of cytosine methylations Patent: WO 0231186-A 28 18-APR-2002; Epigenomics AG (DE)
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                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 432;
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                   DNA
                           Sequence 28 from Patent W00231186.
AX457067
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                                                             AX457067.1 GI:21715849
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synthetic construct
artificial sequences.
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Matches 357; Conserv
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1012 TCACAATTCATTGTAAAAAGGGAGAGTTTTGGTAGGCTCATAATCGCTATAATGTACCT 1071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 TAAACTTGCCATAATAAAAACTCTTTGAAACATACGATATGTTATTCTTTTCATAACTGG 291
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 192929)
Hyman R.W., Fung.F.L., Qin.F., Rowley,D., Mao,J., Tamaki,T., Kurdi,O.B., Conway,A.B. and Davis,R.W.
Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Aug 12, 2000 this sequence version replaced gi:8810446.

* NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pleces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by the finished sequence as soon as it is available and the accession number will be preserved.

1 192929: contig of 192929 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.8%; Score 70.4; DB 2; Length 192929; 13.7%; Pred. No. 0.015;
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/db_xref="taxon:5833"
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17397 c 22111 g 72279 t
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2 (bases 1 to 192929)
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Plasmodium falciparum
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Matches 458; Conservative
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AC115598 1002 S6099 bp DNA linear HTG 21-MAR-2002 Dictyostelium discoideum chromosome 2 map 710700-766797 strain AX4,
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472 ACGTTAGCTCTATAGAAAATATACAAACTAAATCCTTAAAGGAATTTCCTCTATATAAT
                                                                                                    532 AGGAAATCCCTCTCACAGTGAACTGAATTATCCATCTGAATTATCAGTCCACTAATTCCA
                                                                                                                                                                                                                                                                                                              AGCTTATTGTTCATAATTAGCCATGTTGCACCCCTAATTCGAACATTAACTGTAT-CCA
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HTG; HTGS_PHASE2.
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15111. .15393))
/note="ORF_ID:dd_03268"
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17648. .17862)
/notes_orF_lb:dd_00399"
                                                                                                                                                                                                                                       Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb.jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry I
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MATAYVSFILLVGLALSRLTIMKLKAKLDOKIQILNDDFKEKNIITEREVKKEQVSS
MRTKNHILLNIIYNIQLIADQSNSTRAEESLOKEIKKEIQVIEKNPIDKLIKNNYNNS
NNDNNSNNNSSYTQATSKLQQPQSQPIEJRIKNKNNDYQKIEYSLEIIKDFNVNLKN
VDDDDDNNDVEIEMDSMNKANFEMVSNIXSDDKAPLIV"
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/protein_id="AAL92314.1"

/db_xref="GI:19570018"

/translation="MSINKEKTKFNTFRLPTKKXICSCTHNEYSEDLKIPKAIDGVPI
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ISISKSGMFFDYNKYSIKYCVLPDNDITVFINSNNRNPYFGLLEEDMFTMDPFKMQRL
GSPSIESIGFRNIAMKMVIIEFDKLIYKGNQIGIILNDLYTTSDWIEKLSGMDLYMYD
SLINHYGTNNIKMYSLIKSHNIIFNVYDINEINLSNYLLFSNQNLRNHGIFRSCNLNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MNFLYFPNKVSFCIETVDNDEFDNNNSRNSSKATTIDSFINTPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATSINKNDNYKIIENHYDLVIPNYKDGYWVTYSIDSMYSTNQRQVDFIKLHIFKQTNN
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                                                                                                                                                                                                              Submitted (21-MAR-2002) Genome Analysis, Institute of Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agency: Deutsche Forschungsgemeinschaft (DFG).
* NOTE: This is a "working draft' sequence.
* This sequence will be replaced.
* by the finished sequence as soon as it is available and the accession number will be preserved.
                            Sequence and Analysis of Chromosome 2 of Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                (http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                        The Dictyostelium Genome Sequencing Consortium 2 (bases 1 to 56099)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Dictyostelium discoideum"
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                                                                                                                                                                                     Direct Submission
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                                                               Unpublished
                                                                                                                                                        Baumgart, C.
Noegel, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            Funding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                         TITLE
JOURNAL
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JOURNAL
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                                                                                     REMARK
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FEATURES

COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQKGPMTPRTLFSKRESDKKNPSSYIMEDSQYLYILCRGCKMCEKRFQHYMTIKKHLK
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SLGGLSNWASDINLINNSDNNKNNNNNNSTFRNKOLINKYTLKEPWRKGYILRS
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RRKFETLISKSDELIWFWTVWECSKFCIANRLKSPYGSAFQTFEIFEKLLLQLNKDRR
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SDSSQSQEDEDNNVVEGEGGEGGEGDIDELNLVQDSSNGKDAFKSIQGLTVVNQVRLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGTTGCCTAACCATTGAAAATAATAGGCTAAGGTTTTTCCTGATGCGTTTAACTAAAAA
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43.8%; Pred. No. 0.028;
iive 0; Mismatches 681; Indels 15;
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/protein_id="AAL92322.1"
/db_xref="G1:19570026"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein"
/protein_id="AAL92321.1"
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16628 CATATACACCTTTTTACATATACATTTTTTTTTTTTTCACAAAAACTTAAACTTATA 16687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTITGGGATICTIGGAAATTAATTITAATCATCCCAACAGAGAGTTAAAAATTCCAAAAA 16035
                                                                                                                                                                                                                              16216 TTTTGTGATATTGGAATTTATATATATTTTATTTGATTAGTTATTTCAATTGGACTTG 16275
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                                                                                                                                                                                                                                                                                                                                 GCATCTACTATAAGCTCAAACAAATTATCTTTCAAAAATGTTATAATTAACAAGTCA 952
CAATAAAATAGATTAGTGTATTGTTCTCTTCAGTACAATTACTACCATTATGCAATGCTA 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    713 TTTTTCTTGTCCTTCTTGTTTTTTTTTCTAACAAAAIGTTCCAGAATTTTTTAAAAAATA
                                                                                                                                                                                                 TTTGAAAAAACACATAACACTTTGAGTATGATAATATCAACTATTGACTTGTTTTGAAAG
                                                                                                                                                                                                                                                                   833 TAAAGAATCAAATTTTTTTTTTTGTAACTGGACTAATGCACTTTACATCAACTGGATGTTATTT
                                                                                                                                                                                                                                                                                                  653 GCTTATTGTTCATAATTAGCCATGTTGCACCCTAATTCGAACATTAACTGTATCCATA
                                                                                                                                                                                                                                                                                                                                                                                                    953 TCTATAATTCTTTGGATCCAAAAACAAGGAATTCGGAAATTCTGACGATAAATGTCGACT
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15857 AAAAAAAAAAAAAATTAGTAGAAAG-TCCTTTAGTAGTTTTTTTGATTAATTTGACC 15915

SOURCE

TITLE

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Lawson,D., Bowman,S. and Barrell,B.
Direct Submission
Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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HTNNILNYNDHTLKLICNITENNKALLHSNKSNLQKNNILMPSYMQKKGTHIRETIKN
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NNNNNNNNDDVIENMEYPITSKNIYDSIYIPQINIKNIINSEEINNNNNINDNNH
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GINCTVFRAAGATGSGKTYTMLDDKNQNIYQESLELEFTIINEKKCRNIKVLMSFLEV
YNETIRDLLGKERNYTLEVQDGYDAVEKVEYSNLCEIEPNNYEQAMLLINEGYKNRKMSPT
RANKVSSRSHAILQIYVNEILDDNMNTISTRAKLCFVDLAGSBRASATSNKGBRFKE
SSTINGSLLAALNCINSLAANNISTNYRVKKRENSCHTHLKNSLEGNCLYVMIANIND
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KKVDSLKDLYQEEKQFLNNLFDTFLEKNLNYVINSKDVNDNNKSLLEEMIFFKHNENK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oliver,K., Bowman,S., Harris,D., Lawson,D., Quail,M. and Barrell,B. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRTSFQESNNTLKYAFRARNIKLCATVQTNDNKESDIEKILKKNENLQKEYDTLLGKY
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AEGKSESHNKNNKDDIEDNDKDIIKDIHNNNNSSDNNDDEYQSANSPVESDIVKKEKK
                                                                                                                                                                       Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T., Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T., Centles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S., Hornsby, T., Horrocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J., Moule, S., Murphy, L., Oliver, K., Quail, M.A., Rajandream, M.-A., Rutter, S., Skelton, J., Squares, R., Squares, S., Sulston, J.E., Whitehead, S., Woodward, J.R., Newbold, C. and
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//note="PFC0860w (MAL3P7.1), Kinesin-related protein, len:
1200 az; Similarity: to kinesin-related protein.
D.melanogaster kinesin-like protein 674 (TR:P91945) BLAST
Score: 664, sum P(2) = 1.9e-67; 28% identity in 707 aa
overlap, predicted using hexExon, Pfam: match to PF00225
kinesin, Kinesin motor domain Score 311.54"
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On or before May 14, 2001 this sequence version replaced
91:2982540, 91:2982541, 91:2982544, 91:2894453, 91:2894464,
91:2982551, 91:2982556, 91:2982558, 91:2894586,
91:2982566, 91:2894491, 91:2982569, 91:2695974, 91:2894589,
91:2673766, 91:2894496, 91:2982577, 91:2894588, 91:2894589,
91:2982538, 91:2894896, 91:2894880, 91:4725992.
For more information about this sequence or the Malaria Project,
see http://www.sanger.ac.uk/Projects/P_falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The complete nucleotide sequence of chromosome 3 of Plasmodium
stevor, T-complex protein 1 epsilon subunit; telomere; var. Plasmodium falciparum 3D7.
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Plasmodium falciparum 3D7"
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/protein_id="CAB39023.1"
/db_xref="GI:4493964"
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458. .4060
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Nature 400 (6744), 532-538 (1999)
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458. .4060
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                                                                                                                                          (bases 1 to 253305)
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                                                                        ORGANISM
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COMMENT

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indicate splicing"
join(5457..5577,5689..5787,5923..6077,6189..6743)
/gene="PFC0865w, MAL3P7.2"
join(5457..5577,5689..5787,5923..6077,6189..6743)
/gene="PFC0865w, MAL3P7.2"
/note="PFC0865w, (MAL3P7.2"
/note="PFC0865w, (MAL3P7.2"), RNA-binding protein, len: 309
aa; Similarity ed to C.elegans RNA-binding protein
(TR:018318) BLAST Score: 378, sum P(1) = 3.8e-35; 378
identity in 297 aa overlap, predicted using hexExon, Pfam:
match to PF00076 rrm, RNA recognition motif: (a.k.a. RRM,
RBD, or RNP domain) Score 58.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MGLFDKTRNIEKLNEAELKNIGNNDSSWHDQYRDSSYIVIGNLD
NRTFEGDIVYTFSQYGEFIDVNLVRDNETGKSKGYCFLSYADORSTLAVDNRDKYK
LERPLVYDHTLINY PLEKFLLDADDKNEYR PTGAEGGGIGVYNVVESEIKLSKVFDKIK
NKSNEEKKKKLLDEDELWALNFEKSIKKDITSPIGHDERSRHNRGAKEEEEDDDDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      len: 181 aa; Similarity to P. falciparum elongation factor 1.beta, (AAF27524) (276 aa), fasta scores: opt: 366, E(): 1.16-15, 53.2% identity in 141 aa overlap, revised: shortened exon 2, Pfam: match to PF00736 EFIBD, EF-1 guanine nucleotide exchange domain Score 61.10"
                                                                   DDEDDDDDDSVDIKYKRHKEKRKSITTKKYDKKEKHKRKSDHRDKHRRRENHSKHREK
STRKKAKHRRHKHSYDKYSSRSRSYSTSSSTDR
join(7801. 7928.8084. 8334,8392. 8583)
/gene="PFCO870w, MAL3P7.3"
/join(7801. 7928.8084. 8234,8392. 8583)
/gene="PFCO870w, MAL3P7.3"
/note="PFCO870w, MAL3P7.3", putative elongation factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MANTYDELYVPLSYYILQNEGGNTSKIDQANTKKPKKEVINKS
SLIIDIKPYGENTDLDEVLKLVKNITMEGLTWGKAHKKTPFAFGLFKLQVSCVIVDDL
VNTDELIETIENLGLDNEQLQKKKQMDDDEENYDEDDEIGGLVQSAEIISFNKL"
KKIPINMETKKKRTMNGTKDPIHKTPYDINIVGILNKEDVSNKSNDYNTNKNIEKNNY
                                   EKKGEYNPFHNNLTDMQNSILYNIINNNVENSPHSPRMKKNVAKMLLKGNLNTANFIL
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SLELNDDILNIHENDKNSLLYNLHTNIINLKSSEFNINDLYKDVYTENEFENIKNLKI
NPHILKVVKNTEFYKNFIKDIKNLKNENHYTQYFNDDRKKLFFYNFVKNNLVETKYSC
                                                                                                                                                                                                /gene="PFC0860w, MAL3P7.1"
/note="Potential splice donor at 3' end of PFC0860w may
                                                                                                                                       DIHLTSIDTISKIHARDLLKENKRKLENFQENIKHEHKDEVSLYVKKKKIKKKM"
                                                                                                                                                                                                                                                                                                                                           /note="potential splice donor at 3' end of PFCo860w may
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="potential splice donor sequence may indicate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="revised splice donor sequence for exon 2 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein, PFC0875w"
/protein_id="CAB39024.2"
/db_xref="GI:8052275"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative RNA-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative elongation factor"
/protein_id="CAB39068.2"
/db_xref="G1:8052274"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          further splicing of PFC0870w" odf pfC0870w" join(11431. .20416,20578. .20690) gene="PFC0875w, MAL3P7.4" join(11431. .20416,20578. .20690) /gene="PFC0875w, MAL3P7.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:097318"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="SPTREMBL:097319"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="PFC0870w, MAL3P7.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SPTREMBL:097278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAB39067.1"
/db_xref="GI:4494008"
                                                                                                                                                                                                                                                                       indicate splicing"
4057. .4062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                       4028. .4033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFC0870w
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                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                       misc_feature
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IKEFVMNRIFKRNCNDTNNYDNNSNNNNNNDNHNDNHSNNSGINSFNNNNVHNKNI KNDEETSCSONVILYENIFFFETIKFLLYYKNVDKXLNKRTLKENDLDJVQYL NDQIKNLMDEVKKRISISIFCELVKRDIYILDEPFIALDIKTKTKLKFKFDKIKKNNII PICTHDIYEANNFANDIAVIKSGQIIFKGSKNSFQKLIEYKFTLNIOFNGLPNEEQIN NTVDIEMQISEKSNIKEKMLYKETEIDKYYKÖQSDDDNDEKNFNKISQKYILKNLNI KRRPYKIYTESSIFNNDLNILYFFKYFFCNNKONLKGSLQTIAXGQUYZINNKFTNKK NQNEHISEKIQKMNERDYKIELLPTMYZIYEHEKIILLFFKNIELTNVELKYIINLLMLI VNLKODIHINCNQLSGGMKKKVELMINLLKDDKIIFLYKLNDNIDFCSQIYINIILKN LLFTIICMOFSNISSINYIATFLLFFLFSSFRLIIHSGASNILTFFVLLIPHSSFCLS
LLDFTIICMOFSNISSINYIATFLLFFLFSSFRLIIHSGASNILTFFVLLIPHSSFCLS
LLDFTEILIKNNIKIDYKOLFTFFRNISLMHLIICSIVSFVLLICILNYIIXYKKKMN
MLNTYYRGKSKSITNDKRKKOQKTTFFYGNINYDMSEKYPTHOLKDNSNDFMLEGSDE
DDGCYELDTLHKKOYNKGMCLRIFKIRNDRRESNGHPYDIPMIPLHKRONNINNNINNNI
INNNINNNINNNINNOHRNNQCYLLIONVNKFYGKKHALKDVSLTLRSNRIFVLGE YLSQEKIMSALNKKGVIKSPRKVANNYVDGYNVGRISSHESSINDKKKDNNDNNDDD NKNNSVDHIDLEPDILVTNINBETNNRDIIKKNIIKPIKGTRRENKUCETEFRENHI YCTYKINELESLKKLLVANKFKNILTYQLKTIDIYYTYIYTITTARKKLLKNIQDK DIKKILEEIDPLEFLEFQNFKKTENELNNLLLAMKNNHMQPISYNFAYLKDILVRGNENKN LKEKINYIDEPLIEDNLYDSINNYLEKKANHENEISLGTFAFLITEKKADNSDNKEDV ETLETRNDTDVNKEVEININLFYNYTSIHSYAYYTNSLFNMLSDFQNILNKKSGNKNI ILDGSTYDNIKVVEDVKGNCDMNTLLYDKENKYNYLIKDIDNKNIREECNANFRLSKN IINSTNHDDNPYDINMYNNHNKYGKYKNNNNNSFYNMRDDTELTDIEENISSKKKKN KFIEKEFSYNTYRNNKNNDENDEYGEYDNYDDNMIMSNTSNIMKKNIKKQNIEKTCI NFFTTYIKPTLLKLKKDLGSSSFYWYKFIVPLFLLSFGLLIIKCVSLFGKVQNIDLD YSTISSNHLKQSTINYFILYKNEMNNNETLGYNKYNLNDDNIKKNLNNSYDKILKKLE TKQDDNAEESHINNNDHNDNIKDILKLENNEYNYNKLIHENSFNYYNSTINSLLQKYC VSYNNNEEEEDINGNINYNDSNNIYITPKKNNKEEENNFLVKKLKKRIDTLNEPFNIK FHEHFWRDFYINIYVFLSIVIFFCVFFRKREIENRKIFENFHVHQYIHYFQILLLE YLYYFIYILCLFIVLYIFDYKEFLFMSFFCFLLLYGFNIFLSICLFSSLYLHSYILFL FFNFIFCGIISIVIYVLVILSYAYNNEILINLSHVLVCIFRIFDSFALSHVLNIRSLC LAVKRHMKH I DEDI MY EDMSNSNNFVI FGCFKK VY NQLSGDNNLNI SDG I QSVCEDSN SFFNTSGDFVFLLINCIIYLSIVFYKLLQIIPSKERTDKKNESEKTNYEEIILNNSYN VGVQRKKEQKKNRYTFFLKNFYLSNKEYKQPKENYEKNRNPFFYFIQKLFNLKRGNNV DENNTIMGIYKYGEKVDSNNYISEDEININNQLNSEGYLKNDIYMNELNDNYNNDFDD KNNLLTPRYDEINELNKEREITMEYKKTDEKEYQVNNEYINENVGYDEKGGKYKTELK LNDFFIYKMPMKSMKINAFDTFEKNIFRVVVFLCVCLFIVNICFDINKERKINIENFL CCLKINKYYYYYSWLLFYFIILFFYNIIFTLVVYFYVYKCLMNYFILFFLIYFFLMNS NGSGKSTLINIITKMISKDSGEINFFKNSYKNKKKDIYMDVNKNRRNGLCGRICSNGY YFFNDININLKQNFINFNTVDDLSFNIYFNEWYYFSFFIVLEYQFNSFILNYNADILK

Db 177318 AATTATGGATAAAGAATTTTCTAATAAATCAAAACAATGGAGATCCTTTCACGAAAAGC 177377 Db 177378 TATAAGTAAAAGTAAACATCTTTTGGTATCAACTAAAAGGGTTGAAAATATTGAAAATAA 177437 Db 177438 GAATAATCAGTCTAATTTTAATATTAGGAGAAAATTTGATTACAATGATAATGAGGAATA 177497 Db 177618 TITITATATTTATAAGAATTTATTAGGATATTATTATTATTTTGAATATTACAAAAATGAA 177677 384 AGGTTTTTCCTGATGCGTTTAACTAAAAGGAAATAACAAAAGTTATTAGCGATAACCTG 443 444 CGTAAGGTGTCAACAAAATATATTTTGCACGTTAGCTCTATAGAAAATATACAAACTAAA 503 504 TCCTTAAGGAATTTCCTCTATATAATAGGAAATCCCTCTCACAGTGAACTGAATTATC 563 264 TACGATATGTTATTCTTTTCATAACTGGAATATTTTTTGCTTTTTTTAACATTATGAACA 323 204 IGGACCITACACGCACATAAATIGCGGAIAAACTIGCCAIAATAAAAACCTTTGAAACA 324 ATTGAAAAAAAAAGGAAATGAAAAGGTAAGAGTTGCCTAACCATTGAAAATAATAGGCTA 4.7%; Score 69.2; DB 3; Length 253305; 42.6%; Pred. No. 0.021; tive 0; Mismatches 558; Indels 2; Matches 416; Conservative Similarity Query Match Best Local ò δ ŏ οy ò

Search completed: February 23, 2003, 22:57:37 Job time : 6123 secs

177976 ATATATAATATAATCTTTAAACTTGTAGTTAAGGCTTTTTTATTAATACATTGA 178035 Db 178156 TATATTTTCTTTTAATATCATTTAATATTTTGTGATTTGCTTATAAAATATTTTCC 178215 Db 177798 TITITITITICTICCAATTTTTAAAATATTATATGAATATTTTTTCCCTTCATATTTCT 177857 TTCGGAAATTCTGACGATAAATGTCGACTCACAATTCATTGTAAAAAGGGAGAGTTTTGG 1043 924 CTTTCAAAAATGTTAAAATTAACAAGTCATCTATAATTCTTTGGATCCAAAAACAAGGAA 983 744 AAAAATGTTCCAGAATTTTTAAAAAATATTTGAAAAAACACATAACACTTTGAGTATGA 564 CATCTGAATTATCAGTCCACTAATTCCATCAATAAAATAGATTAGTGTATTGTTCTTTC 624 AGTACAATTACTACCATTATGCAATGCTAGCTTATTGTTCATAATTAGCCATGTTGCACA 1104 AAAACCTATAATA 1119 984 op QQ δλ Q ò δλ Ω ò